

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Olopade, Olufunmilayo I.
- (ii) TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHORYLASE
COMPOSITIONS AND METHODS OF USE IN
THE DIAGNOSIS AND TREATMENT OF
PROLIFERATIVE DISORDERS
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Arnold, White & Durkee
 - (B) STREET: P.O. Box 4433
 - (C) CITY: Houston
 - (D) STATE: Texas
 - (E) COUNTRY: United States of America
 - (F) ZIP: 77210
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US Unknown
 - (B) FILING DATE: Concurrently Herewith
 - (C) CLASSIFICATION: Unknown
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/000,831
 - (B) FILING DATE: 02-JUL-1995
 - (C) CLASSIFICATION: Unknown
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Kitchell, Barbara S.
 - (B) REGISTRATION NUMBER: 33,928
 - (C) REFERENCE/DOCKET NUMBER: ARSB:509
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (512) 418-3000
 - (B) TELEFAX: (512) 474-7577

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 122..970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCCGCT CCGCACTGCT CACTCCCGCG CAGTGAGGTT GGCACAGCCA CCGCTCTGTG	60
GCTCGCTTGG TTCCCTTAGT CCCGAGCGCT CGCCCACTGC AGATTCCTTT CCCGTGCAGA	120
C ATG GCC TCT GGC ACC ACC ACC ACC GCC GTG AAG ATT GGA ATA ATT	166
Met Ala Ser Gly Thr Thr Thr Thr Ala Val Lys Ile Gly Ile Ile	
1 5 10 15	
GGT GGA ACA GGC CTG GAT GAT CCA GAA ATT TTA GAA GGA AGA ACT GAA	214
Gly Gly Thr Gly Leu Asp Asp Pro Glu Ile Leu Glu Gly Arg Thr Glu	
20 25 30	
AAA TAT GTG GAT ACT CCA TTT GGC AAG CCA TCT GAT GCC TTA ATT TTG	262
Lys Tyr Val Asp Thr Pro Phe Gly Lys Pro Ser Asp Ala Leu Ile Leu	
35 40 45	
GGG AAG ATA AAA AAT GTT GAT TGC ATC CTC CTT GCA AGG CAT GGA AGG	310
Gly Lys Ile Lys Asn Val Asp Cys Ile Leu Leu Ala Arg His Gly Arg	
50 55 60	
CAG CAC ACC ATC ATG CCT TCA AAG GTC AAC TAC CAG GCG AAC ATC TGG	358
Gln His Thr Ile Met Pro Ser Lys Val Asn Tyr Gln Ala Asn Ile Trp	
65 70 75	
GCT TTG AAG GAA GAG GGC TGT ACA CAT GTC ATA GTG ACC ACA GCT TGT	406
Ala Leu Lys Glu Glu Gly Cys Thr His Val Ile Val Thr Thr Ala Cys	
80 85 90 95	
GGC TCC TTG AGG GAG GAG ATT CAG CCC GGC GAT ATT GTC ATT ATT GAT	454
Gly Ser Leu Arg Glu Glu Ile Gln Pro Gly Asp Ile Val Ile Ile Asp	
100 105 110	
CAG TTC ATT GAC AGG ACC ACT ATG AGA CCT CAG TCC TTC TAT GAT GGA	502
Gln Phe Ile Asp Arg Thr Thr Met Arg Pro Gln Ser Phe Tyr Asp Gly	
115 120 125	
AGT CAT TCT TGT GCC AGA GGA GTG TGC CAT ATT CCA ATG GCT GAG CCG	550
Ser His Ser Cys Ala Arg Gly Val Cys His Ile Pro Met Ala Glu Pro	
130 135 140	
TTT TGC CCC AAA ACG AGA GAG GTT CTT ATA GAG ACT GCT AAG AAG CTA	598
Phe Cys Pro Lys Thr Arg Glu Val Leu Ile Glu Thr Ala Lys Lys Leu	
145 150 155	
GGA CTC CGG TGC CAC TCA AAG GGG ACA ATG GTC ACA ATC GAG GGA CCT	646
Gly Leu Arg Cys His Ser Lys Gly Thr Met Val Thr Ile Glu Gly Pro	
160 165 170 175	
CGT TTT AGC TCC CGG GCA GAA AGC TTC ATG TTC CGC ACC TGG GGG GCG	694
Arg Phe Ser Ser Arg Ala Glu Ser Phe Met Phe Arg Thr Trp Gly Ala	
180 185 190	
GAT GTT ATC AAC ATG ACC ACA GTT CCA GAG GTG GTT CTT GCT AAG GAG	742
Asp Val Ile Asn Met Thr Thr Val Pro Glu Val Val Leu Ala Lys Glu	
195 200 205	
GCT GGA ATT TGT TAC GCA AGT ATC GCC ATG GCG ACA GAT TAT GAC TGC	790
Ala Gly Ile Cys Tyr Ala Ser Ile Ala Met Ala Thr Asp Tyr Asp Cys	

210

215

220

TGG AAG GAG CAC GAG GAA GCA GTT TCG GTG GAC CGG GTC TTA AAG ACC 838
 Trp Lys Glu His Glu Glu Ala Val Ser Val Asp Arg Val Leu Lys Thr
 225 230 235

CTG AAA GAA AAC GCT AAT AAA GCC AAA AGC TTA CTG CTC ACT ACC ATA 886
 Leu Lys Glu Asn Ala Asn Lys Ala Lys Ser Leu Leu Leu Thr Thr Ile
 240 245 250 255

CCT CAG ATA GGG TCC ACA GAA TGG TCA GAA ACC CTC CAT AAC CTG AAG 934
 Pro Gln Ile Gly Ser Thr Glu Trp Ser Glu Thr Leu His Asn Leu Lys
 260 265 270

AAT ATG GCC CAG TTT TCT GTT TTA TTA CCA AGA CAT TAAAGTAGCA 980
 Asn Met Ala Gln Phe Ser Val Leu Leu Pro Arg His
 275 280

TGGCTGCCCCA GGAGAAAAGA AGACATTCTA ATTCCAGTCA TTTTGGGAAT TCCTGCTTAA 1040

CTTGAAAAAA ATATGGGAAA GACATGCAGC TTTCATGCCC TTGCCTATCA AAGAGTATGT 1100

TGTAAGAAAG ACAAGACATT GTGTGTATTA GAGACTCCTG AATGATTTAG ACAACTTCAA 1160

AATACAGAAG AAAAGCAAAT GACTAGTAAA CATGTGGGAA AAAATATTAC ATTTTAAGGG 1220

GGAAAAAAA AACCCACCA TTCTCTTCTC CCCCTATTAA ATTTGCAACA ATAAAGGGTG 1280

GAGGGTAATC TCTACTTTCC TATACTGCCA AAGAATGTGA GGAAGAAATG GGACTCTTTG 1340

GTTATTTATT GATGCGACTG TAAATTGGTA CAGTATTTCT GGAGGGCAAT TTGGTAAAAT 1400

GCATCAAAAG ACTTAAAAAT ACGGACGTCC TTTGGTGCTG GGAAGCTCTAC ATCTAGCAAT 1460

TTCTCTTTAA AACCATATCA GAGATGCATA CAAAGAATTA TATATAAAGA AGGGTGTTTA 1520

ATAATGATAG TTATAATAAT AAATAATTGA AACAATCTGA ATCCCTTGCA ATTGGAGGTA 1580

AATTATGTCT TAGTTATAAT CTAGATTGTG AATCAGCCAA CTGAAAATCC TTTTTCGATA 1640

TTTCAATGTC CTAAAAAGAC ACGGTTGCTC TATATATGAA GTGAAAAAAG GATATGGTAG 1700

CATTTTATAG TACTAGTTTT GCTTTAAAAT GCTATGTAAA TATACAAAAA AACTAGAAAG 1760

AAATATATAT AACCTTGTTA TTGTATTTGG GGGAGGGATA CTGGGATAAT TTTTATTTTC 1820

TTTGAATCTT TCTGTGTCTT CACATTTTTC TACAGTGAAT ATAATCAAAT AGTAAAGGGC 1880

CGTAAAAATA AAAGTGGATT TAGAAAGATC CAGTTCTTGA AAACACTGTT TCTGGTAATG 1940

AAGCAGAATT TAAGTTGGTA ATATTAAGGT GAATGTCATT TAAGGGAGTT ACATCTTTAT 2000

TCTGCTAAAG AAGAGGATCA TTGATTTCTG TACAGTCAGA ACAGTACTTG GGTGTGCAAC 2060

AGCTTTCTGA GAAAAGCTAG GTGTATAATA GTTTAACTGA AAGTTTAACT ATTTAAAAGA 2120

CTAAATGCAC ATTTTATGGT ATCTGATATT TTAAAAAGTA ATGTGAGCTT CTCCTTTTAA 2180

TGAGTTAAAT TATTTTATAC GAGTTGGTAA TTTGTGCCTT TTAATAAAGT GGAAGCTTGC 2240

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Ser	Gly	Thr	Thr	Thr	Thr	Ala	Val	Lys	Ile	Gly	Ile	Ile	Gly	
1				5					10					15		
Gly	Thr	Gly	Leu	Asp	Asp	Pro	Glu	Ile	Leu	Glu	Gly	Arg	Thr	Glu	Lys	
			20					25					30			
Tyr	Val	Asp	Thr	Pro	Phe	Gly	Lys	Pro	Ser	Asp	Ala	Leu	Ile	Leu	Gly	
		35					40					45				
Lys	Ile	Lys	Asn	Val	Asp	Cys	Ile	Leu	Leu	Ala	Arg	His	Gly	Arg	Gln	
	50					55					60					
His	Thr	Ile	Met	Pro	Ser	Lys	Val	Asn	Tyr	Gln	Ala	Asn	Ile	Trp	Ala	
65					70					75					80	
Leu	Lys	Glu	Glu	Gly	Cys	Thr	His	Val	Ile	Val	Thr	Thr	Ala	Cys	Gly	
				85					90					95		
Ser	Leu	Arg	Glu	Glu	Ile	Gln	Pro	Gly	Asp	Ile	Val	Ile	Ile	Asp	Gln	
			100					105					110			
Phe	Ile	Asp	Arg	Thr	Thr	Met	Arg	Pro	Gln	Ser	Phe	Tyr	Asp	Gly	Ser	
		115					120					125				
His	Ser	Cys	Ala	Arg	Gly	Val	Cys	His	Ile	Pro	Met	Ala	Glu	Pro	Phe	
	130					135					140					
Cys	Pro	Lys	Thr	Arg	Glu	Val	Leu	Ile	Glu	Thr	Ala	Lys	Lys	Leu	Gly	
145					150					155					160	
Leu	Arg	Cys	His	Ser	Lys	Gly	Thr	Met	Val	Thr	Ile	Glu	Gly	Pro	Arg	
				165					170					175		
Phe	Ser	Ser	Arg	Ala	Glu	Ser	Phe	Met	Phe	Arg	Thr	Trp	Gly	Ala	Asp	
			180					185					190			
Val	Ile	Asn	Met	Thr	Thr	Val	Pro	Glu	Val	Val	Leu	Ala	Lys	Glu	Ala	
		195					200					205				
Gly	Ile	Cys	Tyr	Ala	Ser	Ile	Ala	Met	Ala	Thr	Asp	Tyr	Asp	Cys	Trp	
	210					215					220					
Lys	Glu	His	Glu	Glu	Ala	Val	Ser	Val	Asp	Arg	Val	Leu	Lys	Thr	Leu	
225					230					235					240	
Lys	Glu	Asn	Ala	Asn	Lys	Ala	Lys	Ser	Leu	Leu	Leu	Thr	Thr	Ile	Pro	

Gln Ile Gly Ser Thr Glu Trp Ser Glu Thr Leu His Asn Leu Lys Asn
260 265 270

Met Ala Gln Phe Ser Val Leu Leu Pro Arg His
275 280

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCGTGAAGG TGAGA

15

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCTTAGATTG GAATA

15

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTGGCAAGG TTAAT

15

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGCAGCCAT CTGAT

15

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTTGCAAGGT ATGG

14

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCATAGGCAT GGA

13

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGAGAGAGG TGTGT

15

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTCTAGGTTC TTATA

15

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGGAAGCAG TAGGT

15

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTCTAGGTTT CGGTG

15

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AACCTGAAGG TAAGT

15

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATCCAGAATA TGGCC

15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTGCTTTTTT AACTC

15